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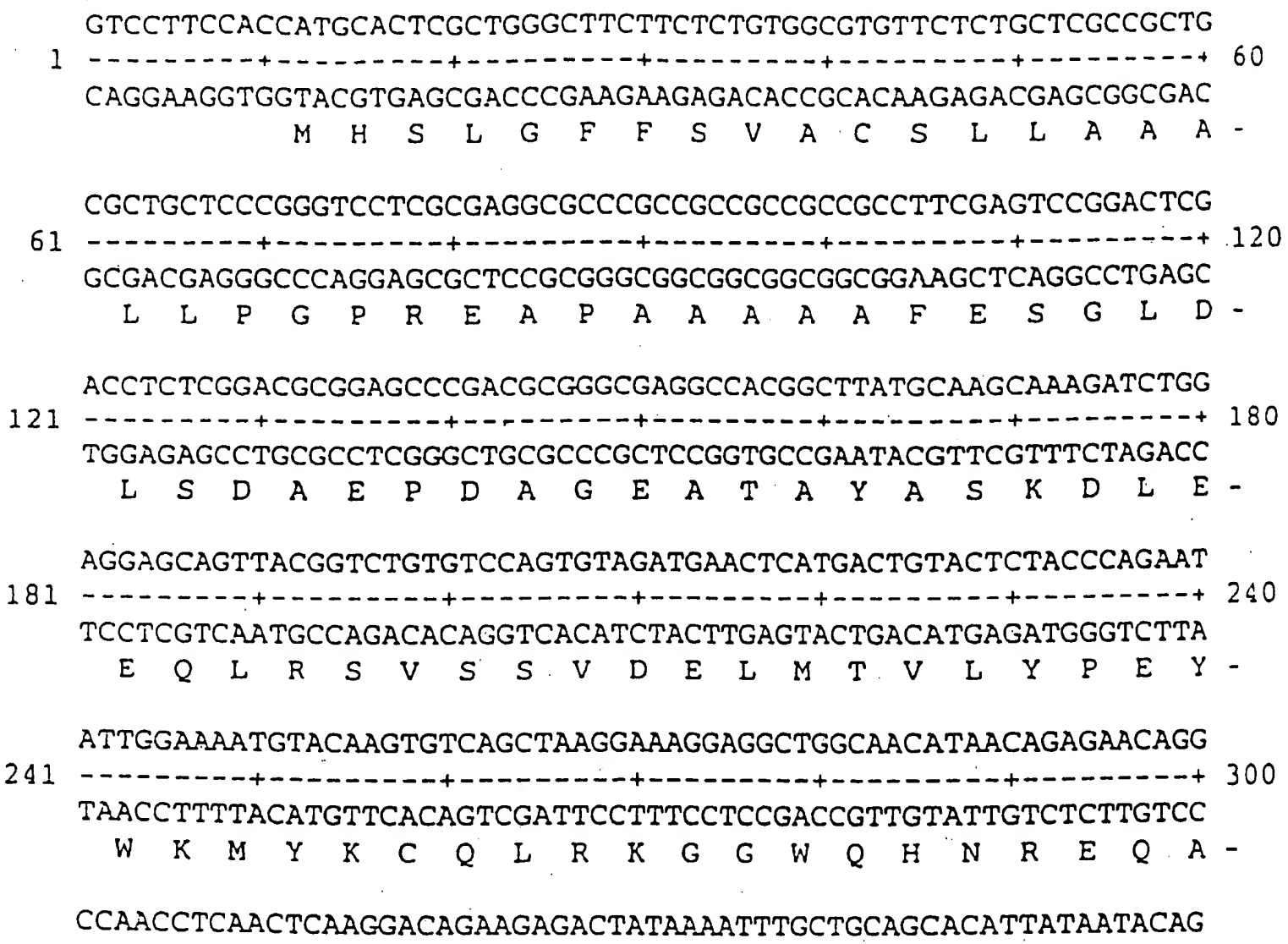

MATCH WITH FIG. 1B

FIG. 1A

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MATCH WITH FIG. 1A

```
301 ---------+---------+---------+---------+---------+---------+ 360
    GGTTGGAGTTGAGTTCCTGTCTTCTCTGATATTTTAAACGACGTCGTGTAATATTATGTC
      N  L  N  S  R  T  E  E  T  I  K  F  A  A  A  H  Y  N  T  E -

    AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT
361 ---------+---------+---------+---------+---------+---------+ 420
    TCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA
      I  L  K  S  I  D  N  E  W  R  K  T  Q  C  M  P  R  E  V  C -

    GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG
421 ---------+---------+---------+---------+---------+---------+ 480
    CATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACAC
      I  D  V  G  K  E  F  G  V  A  T  N  T  F  F  K  P  P  C  V -

    TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA
481 ---------+---------+---------+---------+---------+---------+ 540
    ACAGGCAGATGTCTACACCCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGT
      S  V  Y  R  C  G  G  C  C  N  S  E  G  L  Q  C  M  N  T  S -

    GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCCA
541 ---------+---------+---------+---------+---------+---------+ 600
    CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCCGGGGT
      T  S  Y  L  S  K  T  L  F  E  I  T  V  P  L  S  Q  G  P  K -

    AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG
601 ---------+---------+---------+---------+---------+---------+ 660
    TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTGACCTAC
      P  V  T  I  S  F  A  N  H  T  S  C  R  C  M  S  K  L  D  V -
```

MATCH WITH FIG. 1C

FIG. 1B

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MATCH WITH FIG. 1B

```
    TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
661 ---------+---------+---------+---------+---------+---------+ 720
    AAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGGACGGTCGTTGTGATGGTGTCACAG
      Y  R  Q  V  H  S  I  I  R  R  S  L  P  A  T  L  P  Q  C  Q -

    AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
721 ---------+---------+---------+---------+---------+---------+ 780
    TCCGTCGCTTGTTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCTACGG
      A  A  N  K  T  C  P  T  N  Y  M  W  N  N  H  I  C  R  C  L -

    TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
781 ---------+---------+---------+---------+---------+---------+ 840
    ACCGAGTCCTTCTAAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
      A  Q  E  D  F  M  F  S  S  D  A  G  D  D  S  T  D  G  F  H -

    ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG
841 ---------+---------+---------+---------+---------+---------+ 900
    TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC
      D  I  C  G  P  N  K  E  L  D  E  E  T  C  Q  C  V  C  R  A -

    CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT
901 ---------+---------+---------+---------+---------+---------+ 960
    GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTTCTTGATCTGTCTTTGAGTACGGTCA
      G  L  R  P  A  S  C  G  P  H  K  E  L  D  R  N  S  C  Q  C -

    GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTTGATGAAA
961 ---------+---------+---------+---------+---------+---------+ 1020
    CACAGACATTTTTGTTTGAGAAGGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT
```

MATCH WITH FIG. 1D

FIG. 1C

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MATCH WITH FIG. 1C

```
      V  C  K  N  K  L  F  P  S  Q  C  G  A  N  R  E  F  D  E  N -

      ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
1021  ---------+---------+---------+---------+---------+---------+ 1080
      TGTGTACGGTCACACATACATTTTCTTGGACGGGGTCTTTAGTTGGGGATTTAGGACCTT
        T  C  Q  C  V  C  K  R  T  C  P  R  N  Q  P  L  N  P  G  K -

      AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC
1081  ---------+---------+---------+---------+---------+---------+ 1140
      TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTTCCTTTCTTCAAGG
        C  A  C  E  C  T  E  S  P  Q  K  C  L  L  K  G  K  K  F  H -

      ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGC
1141  ---------+---------+---------+---------+---------+---------+ 1200
      TGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG
        H  Q  T  C  S  C  Y  R  R  P  C  T  N  R  Q  K  A  C  E  P -

      CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC
1201  ---------+---------+---------+---------+---------+---------+ 1260
      GTCCTAAAAGTATATCACTTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG
        G  F  S  Y  S  E  E  V  C  R  C  V  P  S  Y  W  Q  R  P  Q -

      AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT
```

MATCH WITH FIG. 1E

FIG. 1D

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MATCH WITH FIG. 1D

```
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA
       M   S   *

     TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCATGCTAACAAAGACA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     ACGGTGTCATCTTGACAGACACTTGTCTCTCTGGGAACACCCAGGTACGATTGTTTCTGT

     AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC

     CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC
1441 ---------+---------+---------+---------+---------+---------+ 1500
     GTTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCGGTTCTAAAAGGAG

     TTGTGATTTCTTTAAAAGAATGACTATATAATTTATTTCCACTAAAAATATTGTTTCTGC
1501 ---------+---------+---------+---------+---------+---------+ 1560
     AACACTAAAGAAATTTTCTTACTGATATATTAAATAAAGGTGATTTTTATAACAAAGACG

     ATTCATTTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT
1561 ---------+---------+---------+---------+---------+---------+ 1620
     TAAGTAAAAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAATATAGTA

     GCAAAATATGTTTAAAATAAAATGAAAATTGTATTTATAAAAAAAAAAAAAAAA
1621 ---------+---------+---------+---------+---------+---- 1674
     CGTTTTATACAAATTTTATTTTACTTTTAACATAAATATTTTTTTTTTTTTTTT
```

FIG. 1E

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```
                .         .         .         .         .         .
  1  CGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
     ---------+---------+---------+---------+---------+---------+---------+
                .         .         .         .         .         .
 71  AGATGAACTCATGACTGTACTCTACCCAGAATATTGGAAAATGTACAAGTGTCAGCTAAG
     ---------+---------+---------+---------+---------+---------+---------+
                M   T   V   L   Y   P   E   Y   W   K   M   Y   K   C   Q   L   R
                .         .         .         .         .         .
121  GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
     ---------+---------+---------+---------+---------+---------+---------+
                K   G   G   W   Q   H   N   R   E   Q   A   N   L   N   S   R   T   E   E   T
                .         .         .         .         .         .
181  TATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
     ---------+---------+---------+---------+---------+---------+---------+
                I   K   F   A   A   A   H   Y   N   T   E   I   L   K   S   I   D   N   E   W
                .         .         .         .         .         .
241  GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT
     ---------+---------+---------+---------+---------+---------+---------+
                R   K   T   Q   C   M   P   R   E   V   C   I   D   V   G   K   E   F   G   V
                .         .         .         .         .         .
301  CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCTG
     ---------+---------+---------+---------+---------+---------+---------+
                A   T   N   T   F   F   K   P   P   C   V   S   V   Y   R   C   G   G   C   C
```

FIG. 2A

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```
361  CAATAGTGAGGGGCTGCAGTGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATT
     N  S  E  G  L  Q  C  M  N  T  S  T  S  Y  L  S  K  T  L  F

421  TGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTTGCCAATCA
     E  I  T  V  P  L  S  Q  G  P  K  P  V  T  I  S  F  A  N  H

481  CACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
     T  S  C  R  C  M  S  K  L  D  V  Y  R  Q  V  H  S  I  I  R

541  ACGTTCCCTGCCAGCAACACTACCACAGTGTCAGGCAGCGAACAAGACCTGCCCCACCAA
     R  S  L  P  A  T  L  P  Q  C  Q  A  A  N  K  T  C  P  T  N

601  TTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTC
     Y  M  W  N  N  H  I  C  R  C  L  A  Q  E  D  F  M  F  S  S

661  GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCT
     D  A  G  D  D  S  T  D  G  F  H  D  I  C  G  P  N  K  E  L
```

FIG. 2B

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```
721  GGATGAAGAGACCTGTCAGTGTGTCTGCAGAGCGGGGCTTCGGCCTGCCAGCTGTGGACC
     ---------+---------+---------+---------+---------+---------+
      D  E  E  T  C  Q  C  V  C  R  A  G  L  R  P  A  S  C  G  P

781  CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAAAACAAACTCTTCCCCAG
     ---------+---------+---------+---------+---------+---------+
      H  K  E  L  D  R  N  S  C  Q  C  V  C  K  N  K  L  F  P  S

841  CCAATGTGGGGCCAACCGAGAATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAAC
     ---------+---------+---------+---------+---------+---------+
      Q  C  G  A  N  R  E  F  D  E  N  T  C  Q  C  V  C  K  R  T

901  CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCC
     ---------+---------+---------+---------+---------+---------+
      C  P  R  N  Q  P  L  N  P  G  K  C  A  C  E  C  T  E  S  P

961  ACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGACG
     ---------+---------+---------+---------+---------+---------+
      Q  K  C  L  L  K  G  K  K  F  H  H  Q  T  C  S  C  Y  R  R

1021 GCCATGTACGAACCGCCAGAAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG
     ---------+---------+---------+---------+---------+---------+
      P  C  T  N  R  Q  K  A  C  E  P  G  F  S  Y  S  E  E  V  C
```

FIG. 2C

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```
1081  TCGTTGTGTCCCTTCATATTGGCAAAGACCACAAATGAGCTAAGATTGTACTGTTTTCCA
      ---------+---------+---------+---------+---------+---------+
       R  C  V  P  S  Y  W  Q  R  P  Q  M  S

1141  GTTCATCGATTTTCTATTATGGAAAACTGTGTTGCCACAGTAGAACTGTCTGTGAACAGA
      ---------+---------+---------+---------+---------+---------+

1201  GAGACCCTTGTGGGTCCATGCTAACAAAGACAAAAGTCTGTCTTTCCTGAACCATGTGGA
      ---------+---------+---------+---------+---------+---------+

1261  TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCTCTTGTAAAGACTGGTTTT
      ---------+---------+---------+---------+---------+---------+

1321  CTGCCAATGACCAAACAGCCAAGATTTTCCTCTTGTGATTTCTTTAAAAGAATGACTATA
      ---------+---------+---------+---------+---------+---------+

1381  TAATTTATTTCCACTAAAAATATTGTTTCTGCATTCATTTTTATAGCAACAACAATTGGT
      ---------+---------+---------+---------+---------+---------+

1441  AAAACTCACTGTGATCAATATTTTTATATCATGCAAAATATGTTTAAAATAAAATGAAAA
      ---------+---------+---------+---------+---------+---------+

1501  TTGTATTATAAAAAAAAAAAAAAA
      ---------+---------+------
```

FIG. 2D

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```
          1                                                  50
Pdgfa .MRTLACLLL LGCGYLAHVL AEEAEIPREV IERLARSQIH SIRDLQRLLE
Pdgfb MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLQRLLH
 Vegf .....MNFLL SWVHWSLALL LY..... ..... .LHHAKWSQA
Vegf2 .......MTV LYPEYWKMYK CQ..... ..... .LRKGGWQHN

          51                                                 100
Pdgfa IDSVGSEDSL DTSLRAHGVH ATKHVPEKRP LPIRRKRSI. .....EEAVP
Pdgfb GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI
 Vegf APMAE..... ......GGGQ NHHEVVKFMD .VYQR..... .....
Vegf2 REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK..... .....

          101                                                150
Pdgfa AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRCTGCC NTSSVKCQPS
Pdgfb AECKTRTEVF EISRRLIDRT NANFLVWPPC VEVQRCSGCC NNRNVQCRPT
 Vegf SYCHPIETLV DIFQEYPDEI ..EYIFKPSC VPLMRCGGCC NDEGLECVPT
Vegf2 TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

          151                                                200
Pdgfa RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECAC.... AT.....
Pdgfb QVQLRPVQVR KIEIVRKKPI FKKATVTLED HLACKC.... ETVAAARPVT
 Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCECRPKK DRARQEKKSV
Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII
```

FIG. 3A

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```
      201                                                        250
Pdgfa ....TSLNPD YREEDTDVR. ..... ..... .....
Pdgfb RSPGGSQEQR AKTPQTRVTI RTVRVRRPPK GKHRKFKHTH DKTALKETLG
 Vegf RGK..... .GKGQKRKRK KSRYKSWSVY VGARCCLMPW SLPGPHP...
Vegf2 RRSLPATLPQ CQAANKTCPT NYMWNNHICR CLAQEDFMFS SDAGDDSTDG

      251                                                        300
Pdgfa ..... ..... ..... ..... .....
Pdgfb A..... ..... ..... ..... .....
 Vegf ....CGP... ..... .....CSE RRKHLFVQDP QTCKCSCKNT
Vegf2 FHDICGPNKE LDEETCQCVC RAGLRPASCG PHKEL...DR NSCQCVCKNK

      301                                                        350
Pdgfa ..... ..... ..... ..... .....
Pdgfb ..... ..... ..... ..... .....
 Vegf ..DSRCKARQ LELNERTCRC DKPRR..... ..... .....
Vegf2 LFPSQCGANR .EFDENTCQC VCKRTCPRNQ PLNPGKCACE CTESPQKCLL

      351                                                  398
Pdgfa ..... ..... ..... ..... .....
Pdgfb ..... ..... ..... ..... .....
 Vegf ..... ..... ..... ..... .....
Vegf2 KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPQMS
```

FIG. 3B

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PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLWING TABLE				
	PDGFα	PDGFβ	VEGF	VEGF2
PDGFα				
PDGFβ	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

FIG.4

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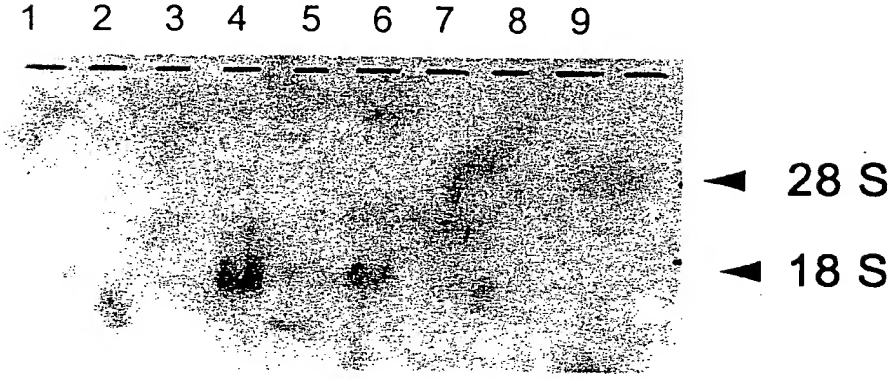
Expression of VEGF2 mRNA in Human Breast Tumor Cells



Lane 1. normal breast tissue
Lane 2. breast tumor tissue
Lane 3-9. breast tumor cell lines.

FIG.5

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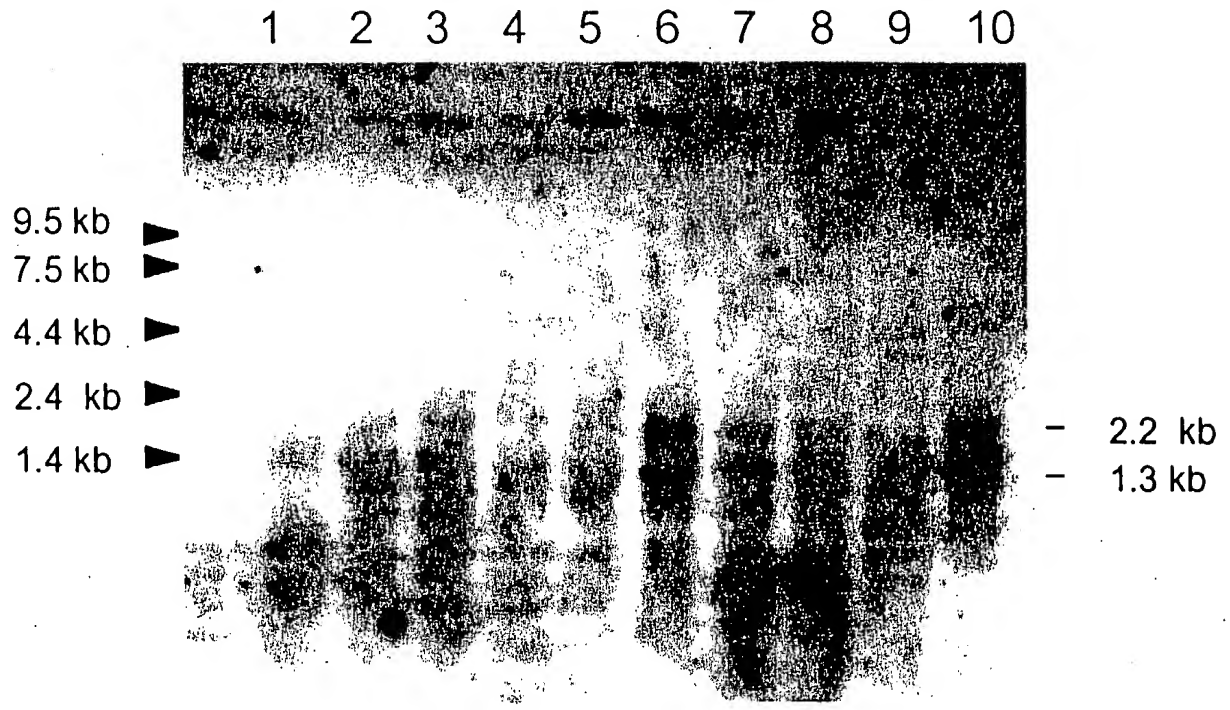

1.	ovary	6.	lung
2.	testes	7.	spleen
3.	gall bladder	8.	prostate
4.	kidney	9.	Hippocampus
5.	liver	10.	heart

Expression of VEGF2 mRNA in human adult tissues.

FIG.6

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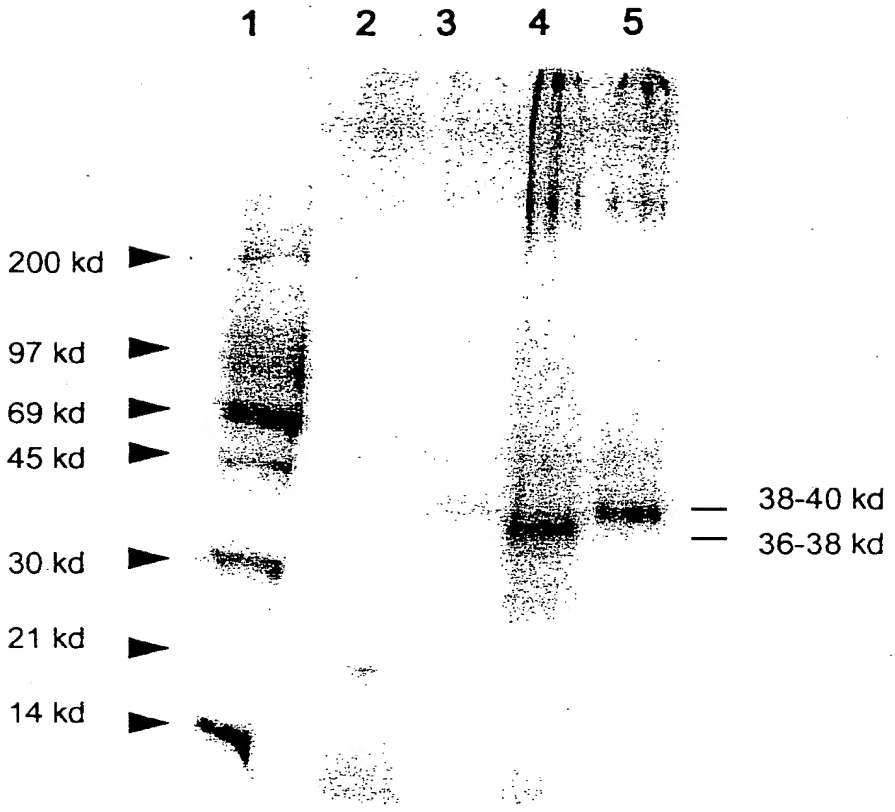
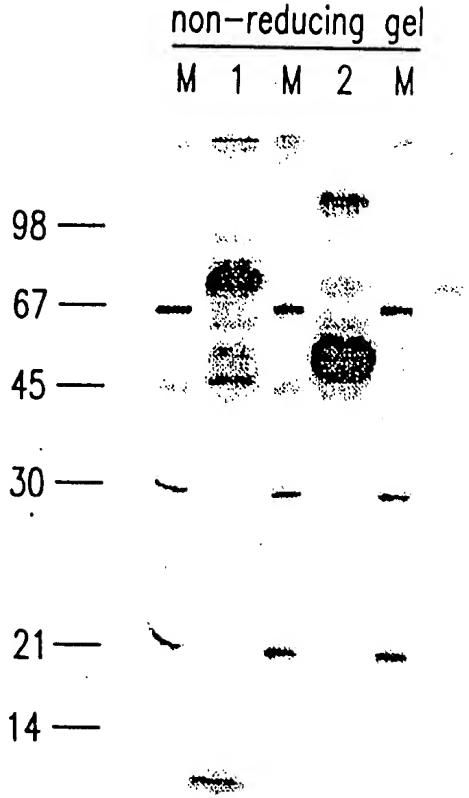


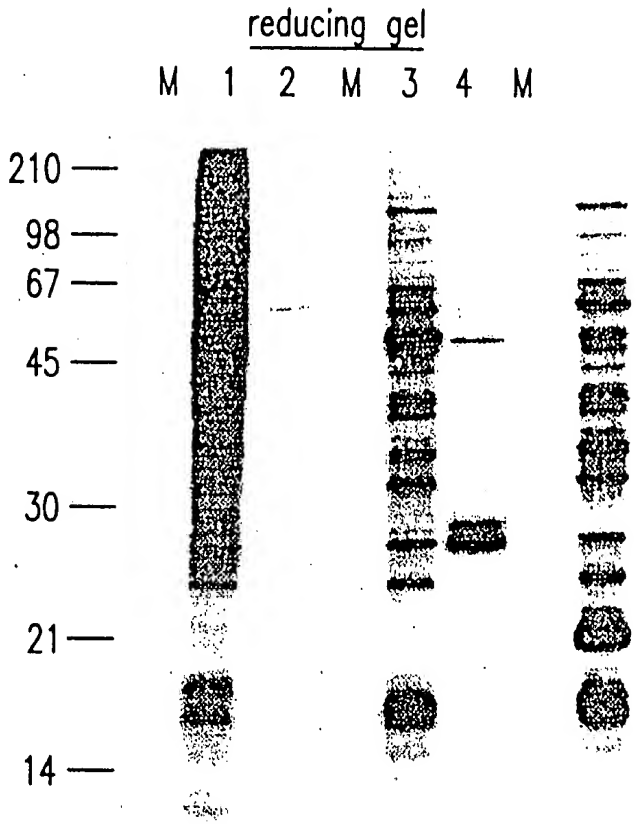
Lane 1: 14-C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse & forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

FIG.7



Lane M Marker
Lane 1 vector medium
Lane 2 VEGF2 medium

FIG.8A



Lane M: Marker
Lane 1: vector Cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 Cytoplasm
Lane 4: VEGF2 medium

FIG.8B

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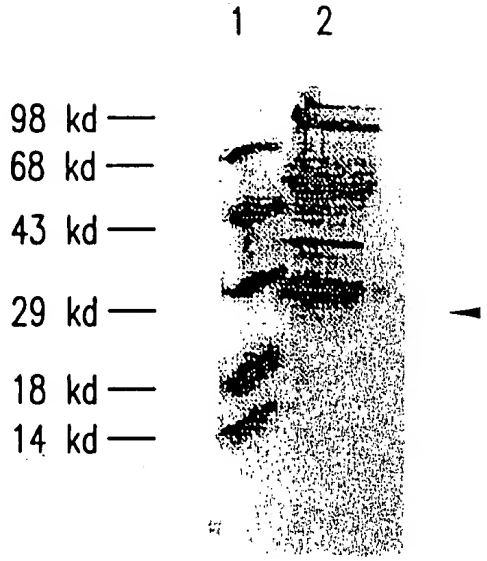

Lane 1: Molelular weight marker
Lane 2: Precipitates containing VEGF2.

FIG.9

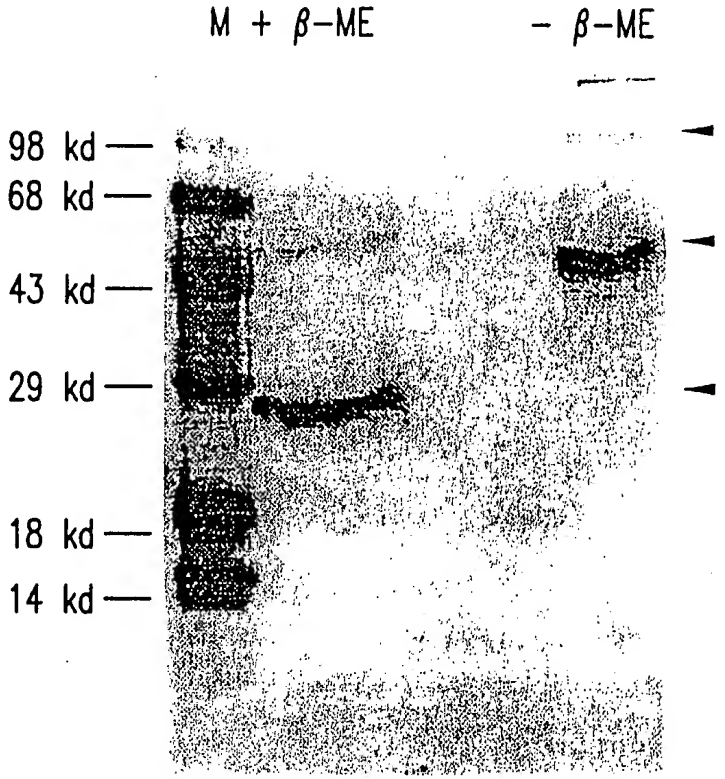

FIG.10

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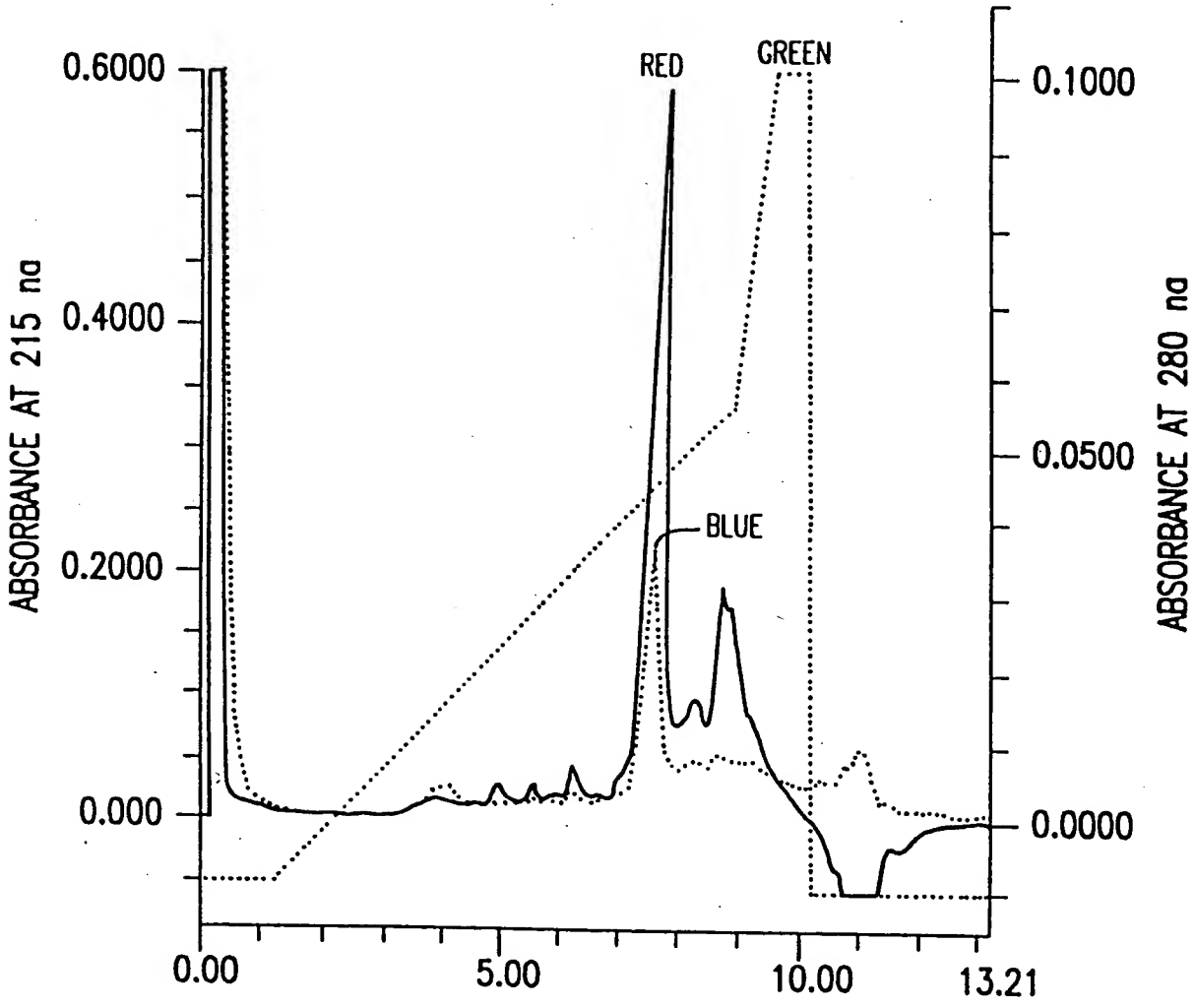

FIG. 11

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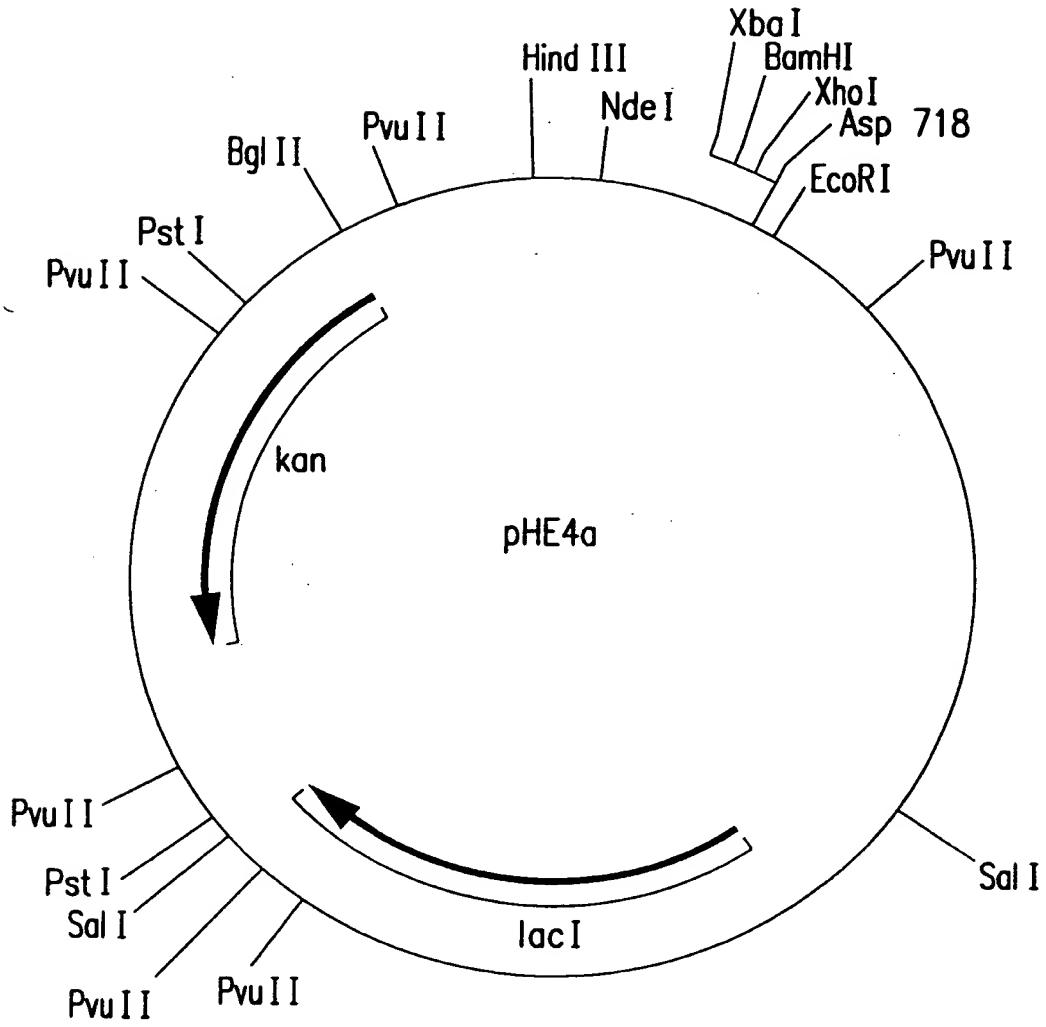

FIG.12

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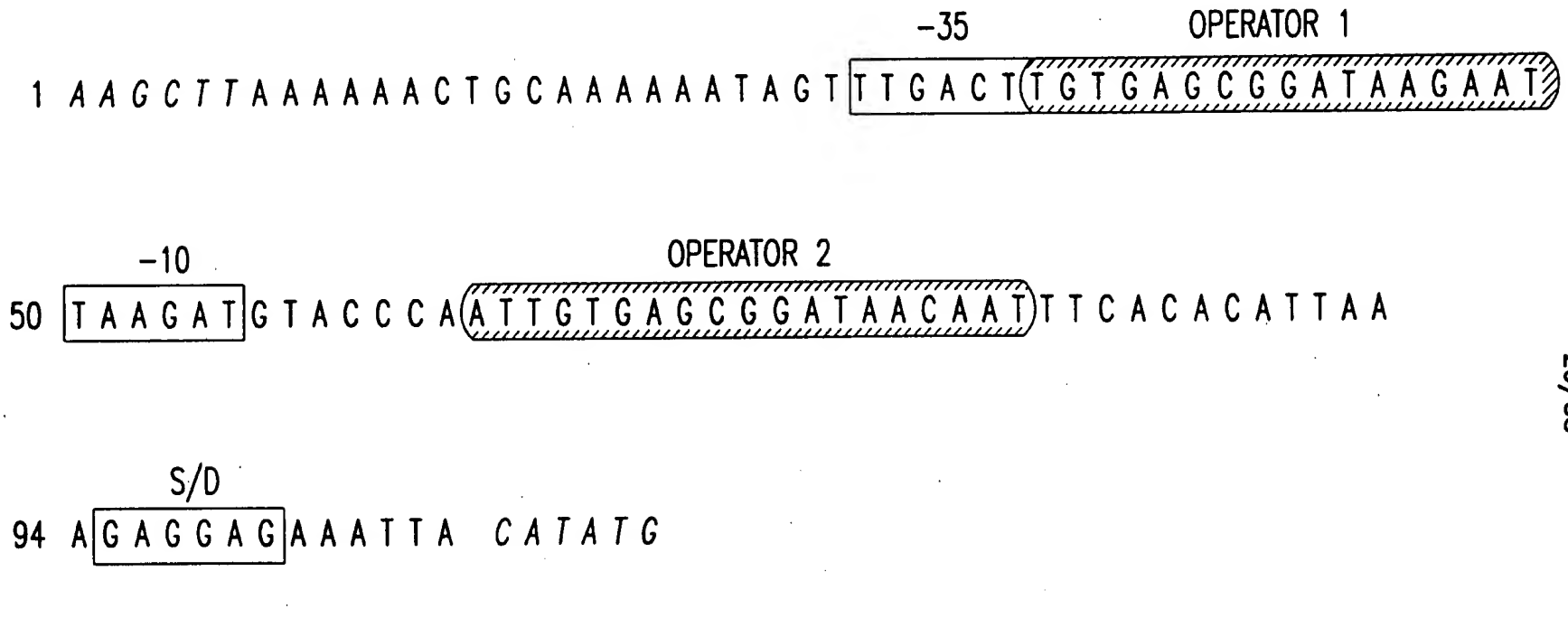

FIG.13

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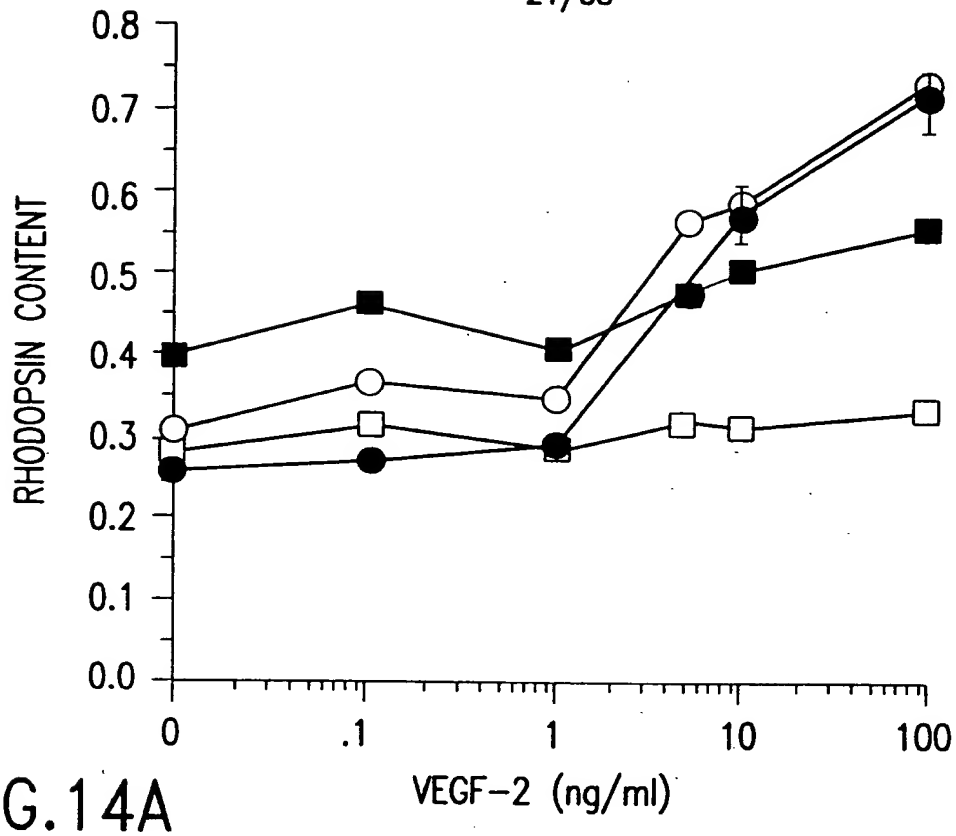

FIG.14A

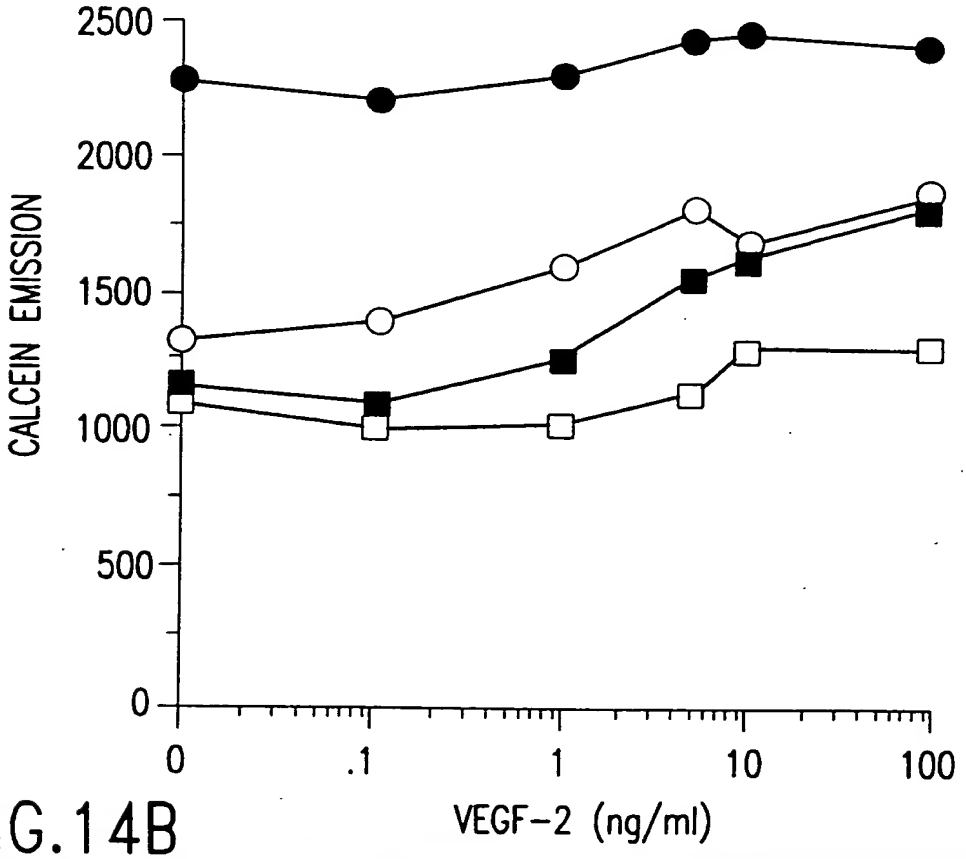

FIG.14B

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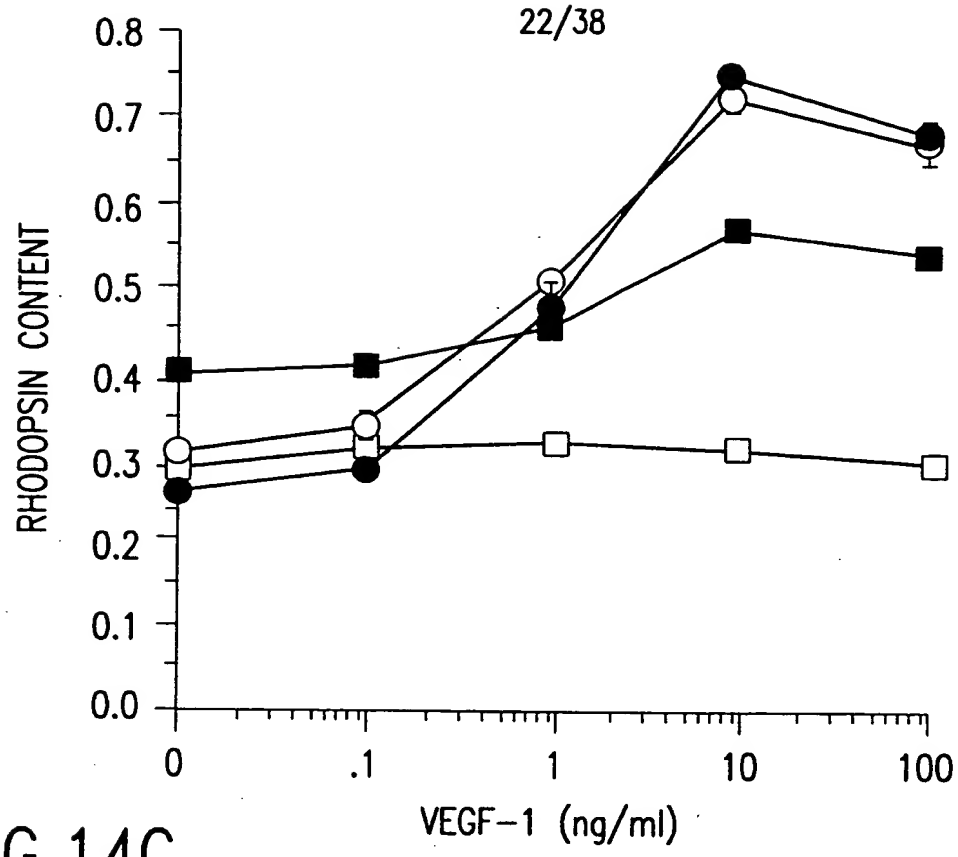

FIG.14C

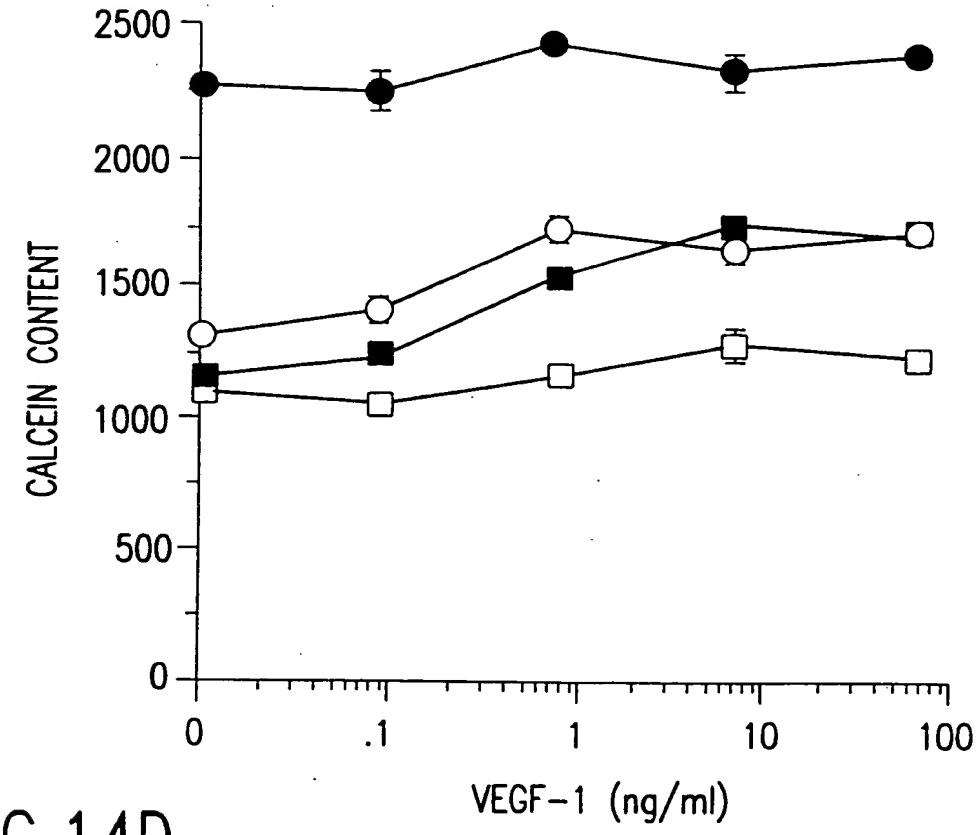

FIG.14D

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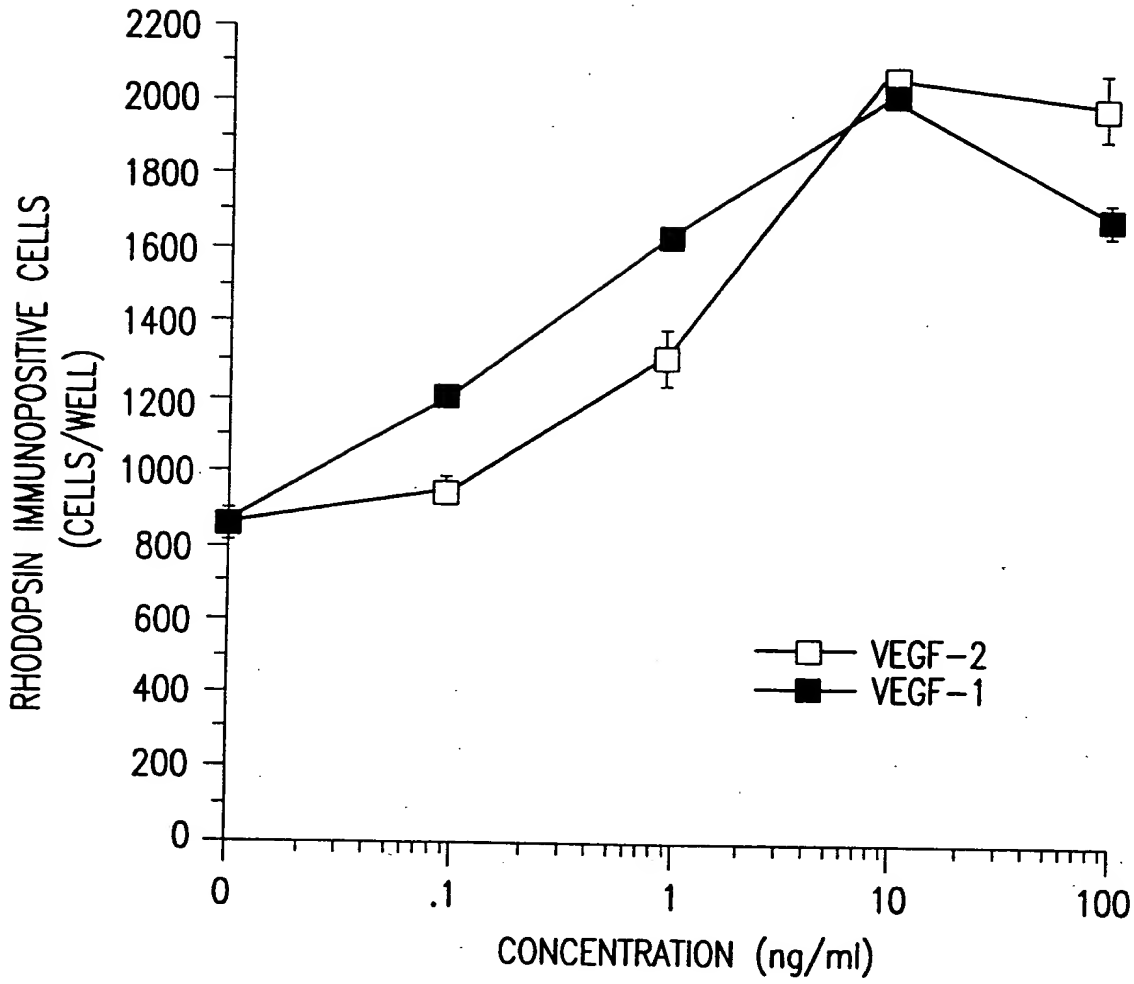

FIG.15

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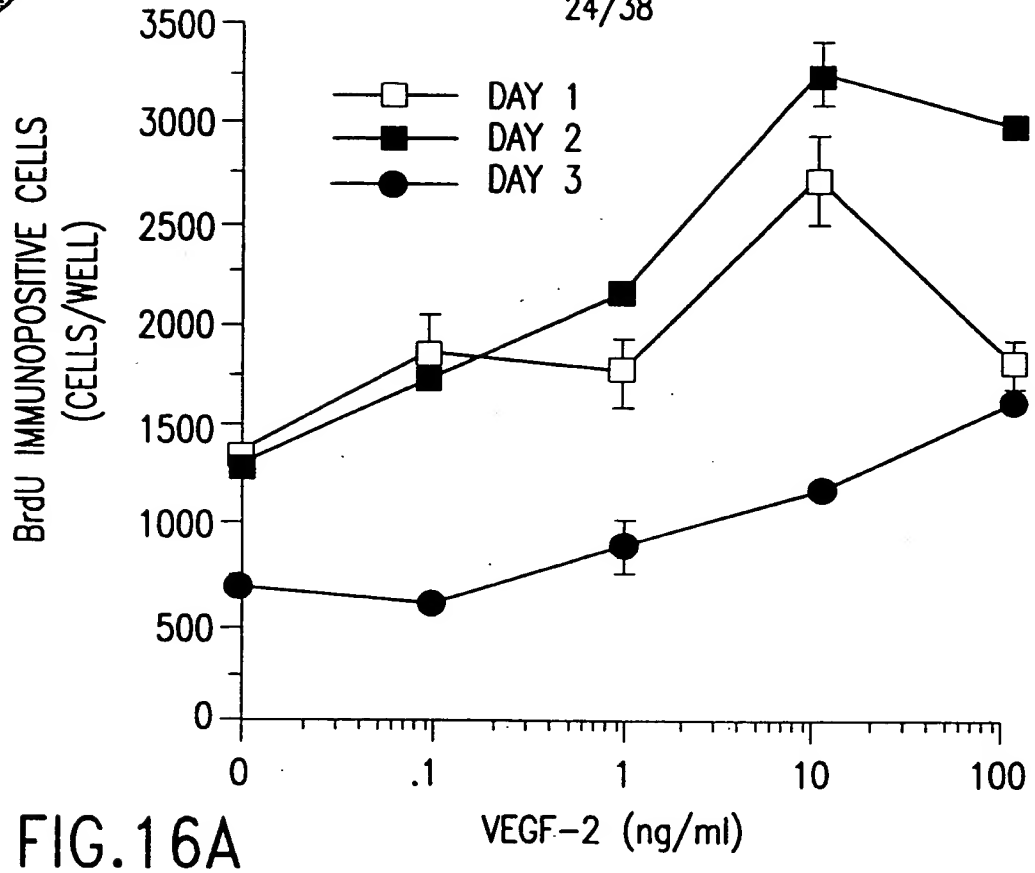

FIG.16A

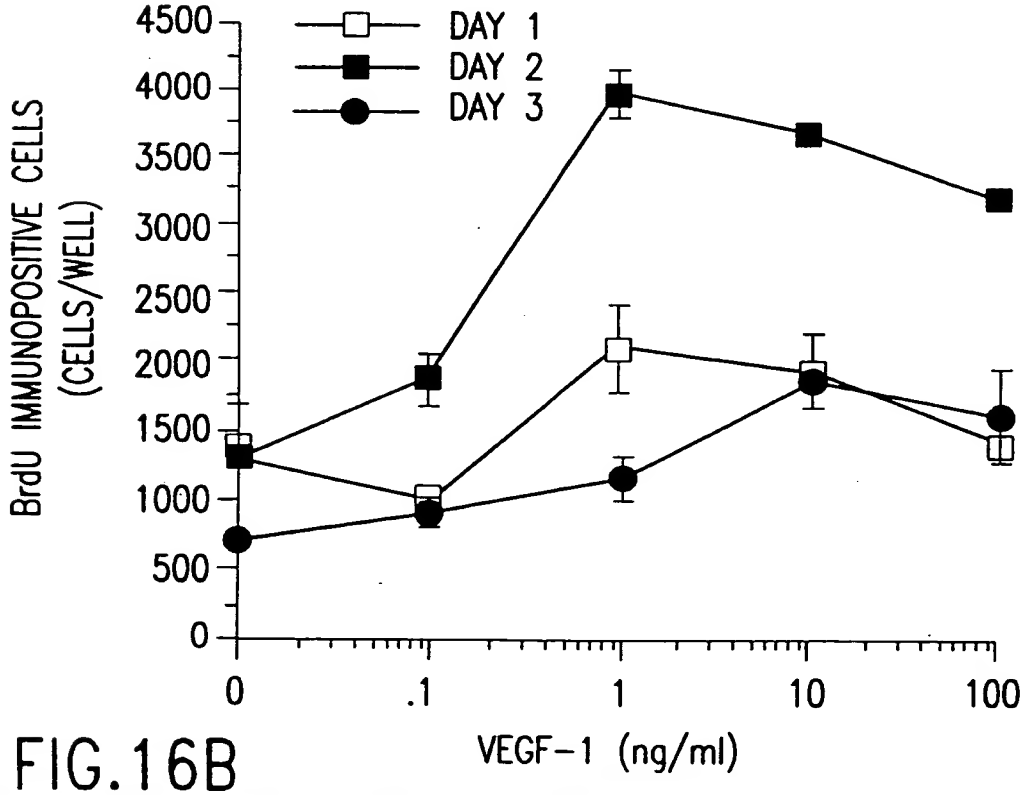

FIG.16B

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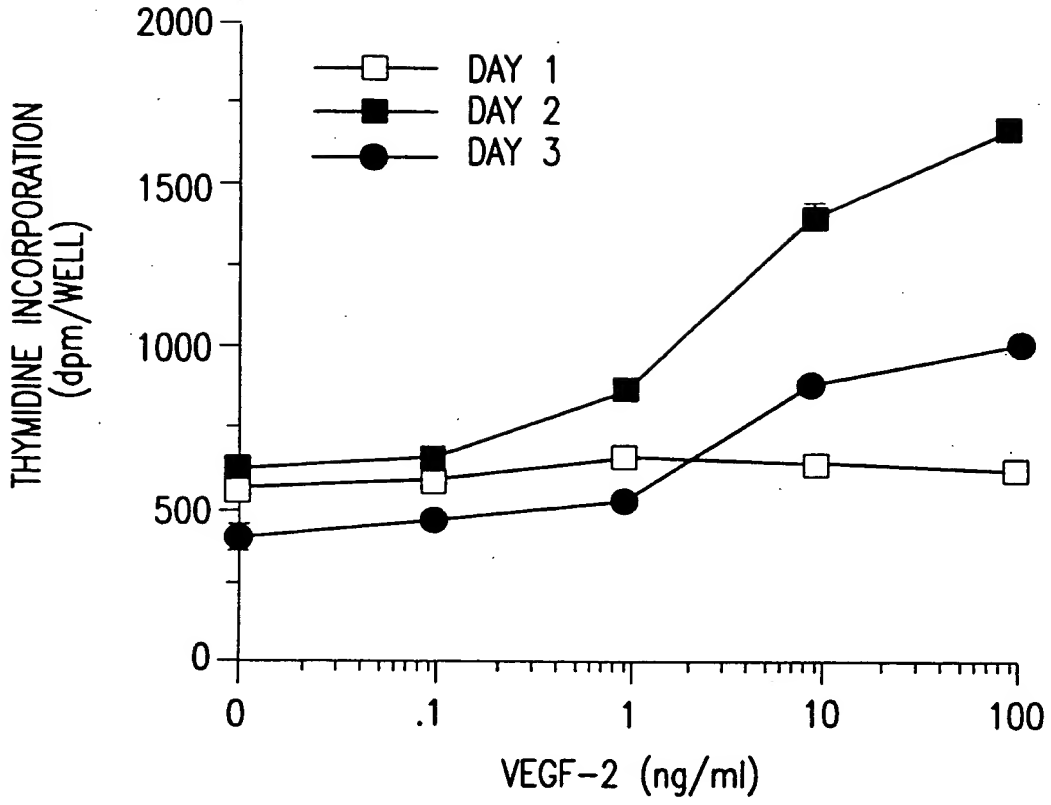

FIG.16C

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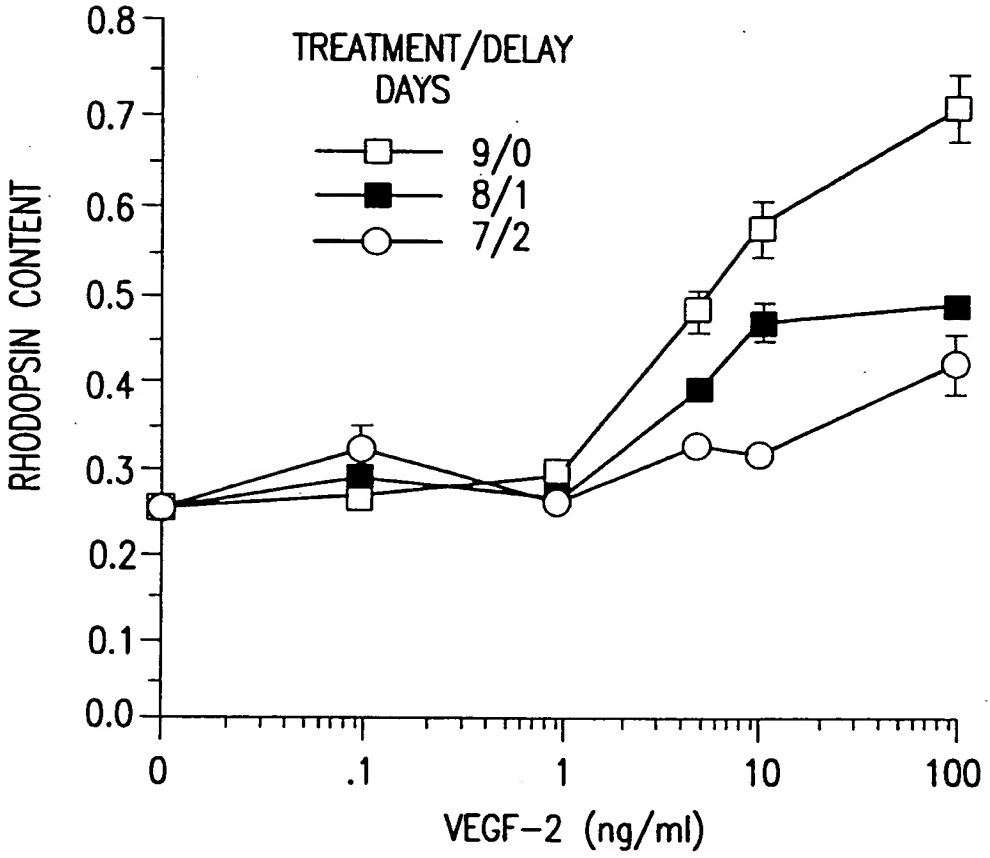

FIG.17A

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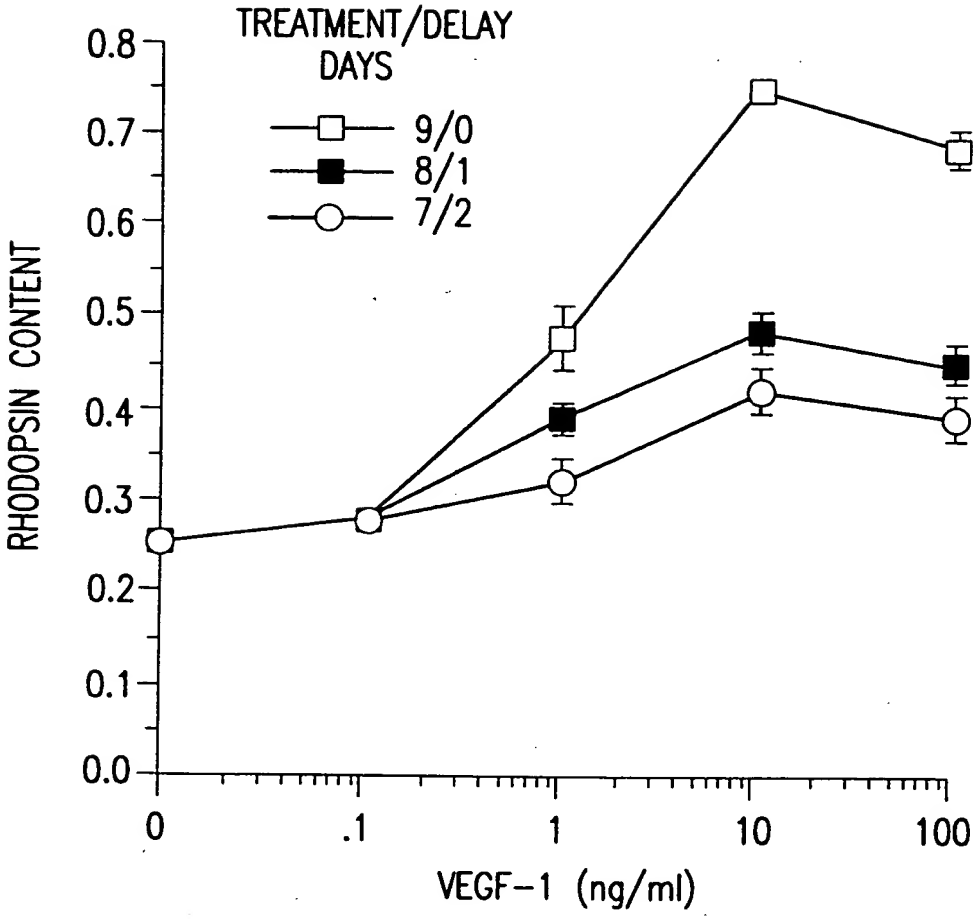

FIG.17B

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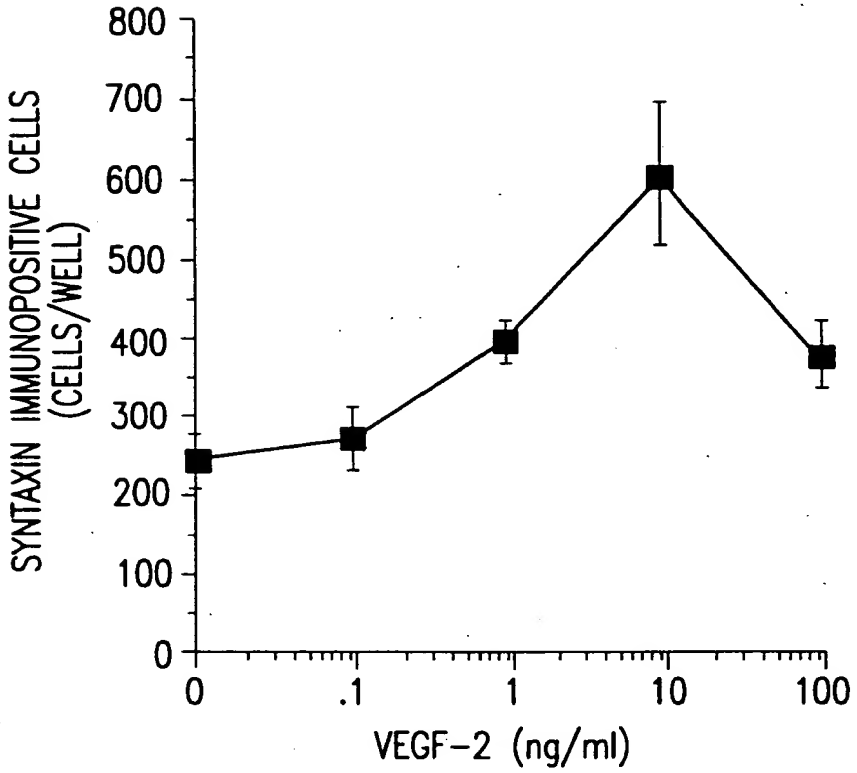

FIG.18A

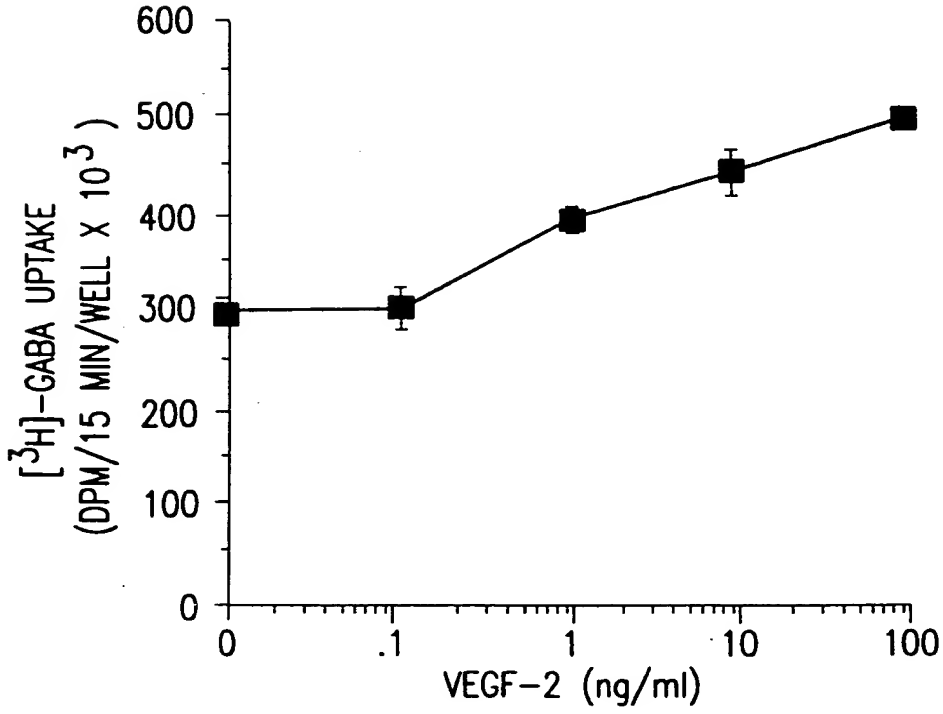

FIG.18B

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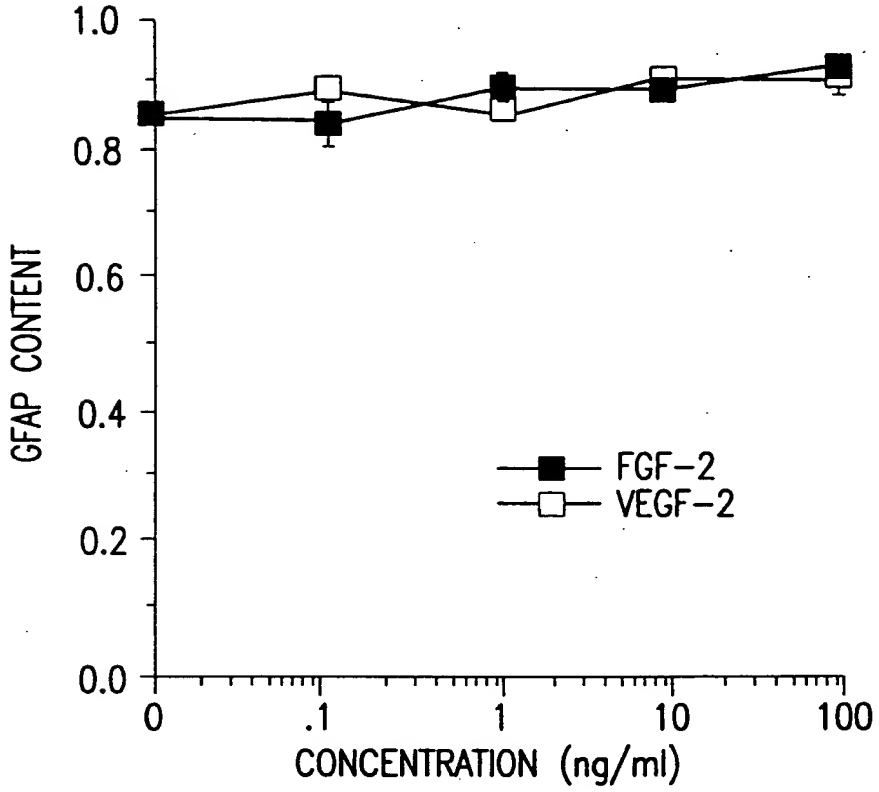

FIG.18C

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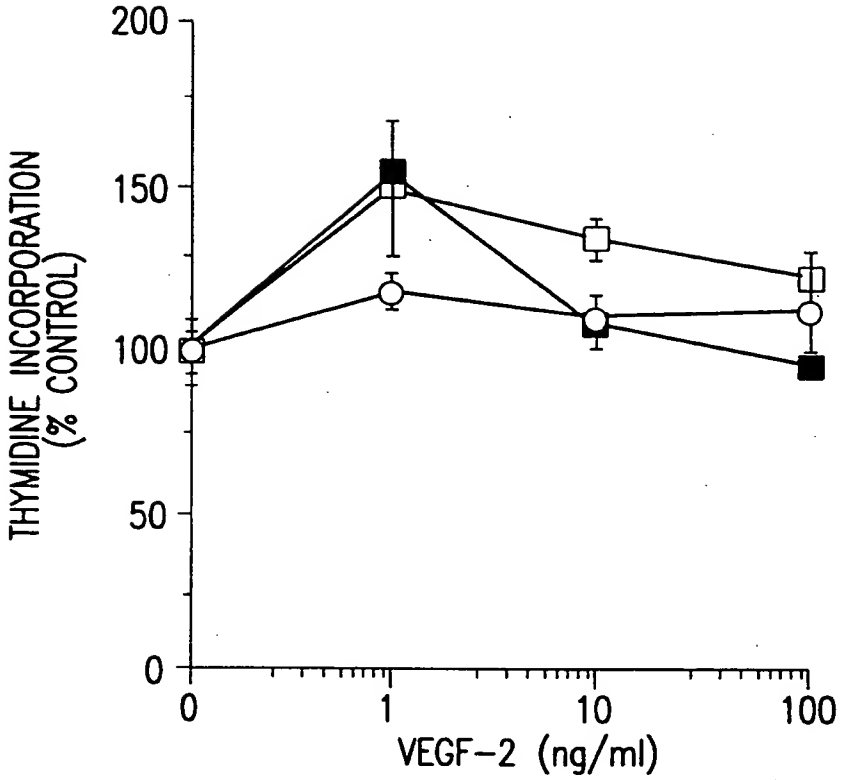

FIG.19A

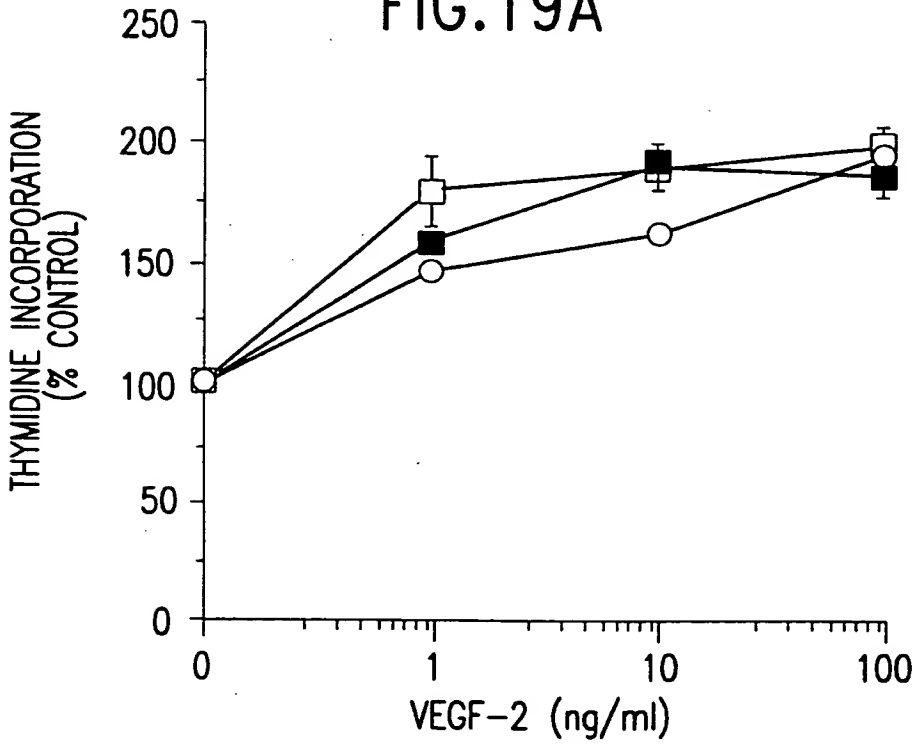

FIG.19B

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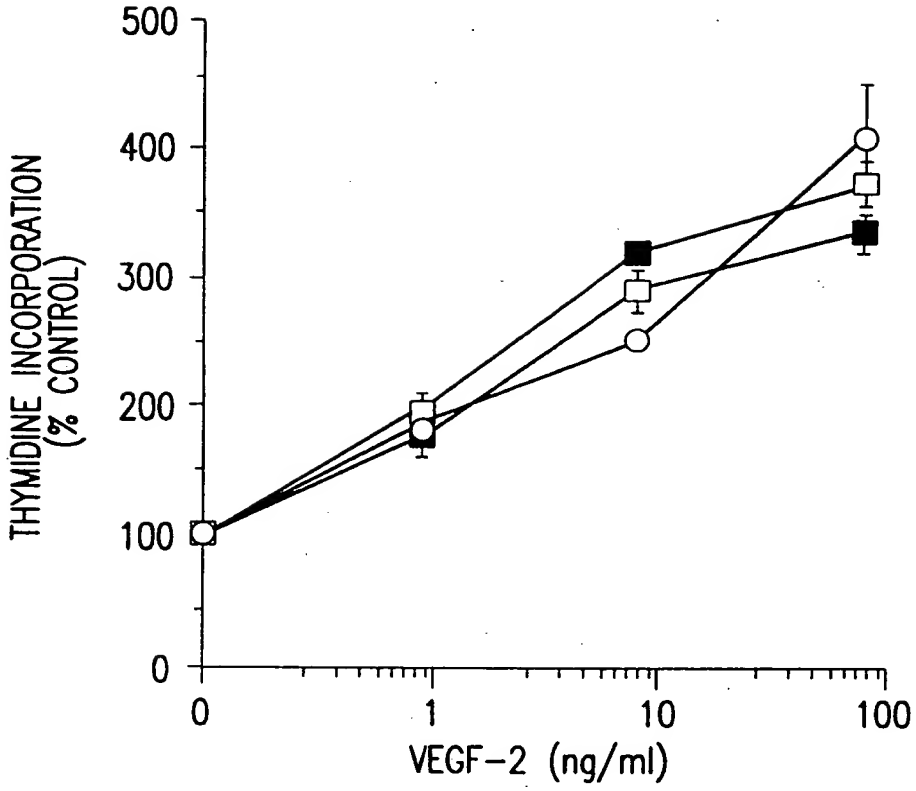

FIG.19C

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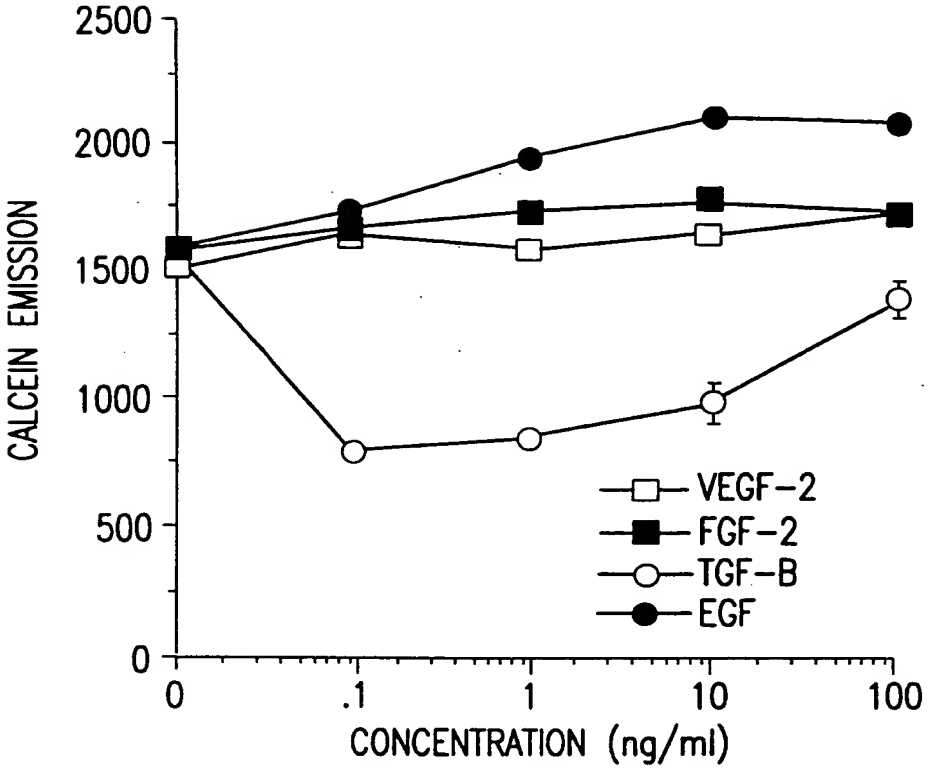

FIG.20A

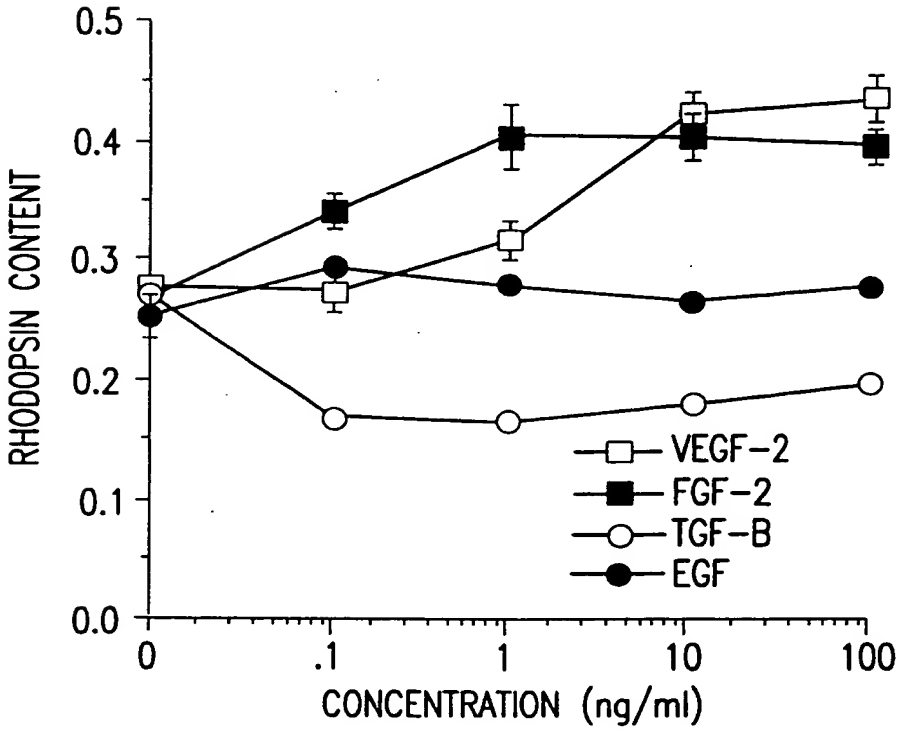

FIG.20B

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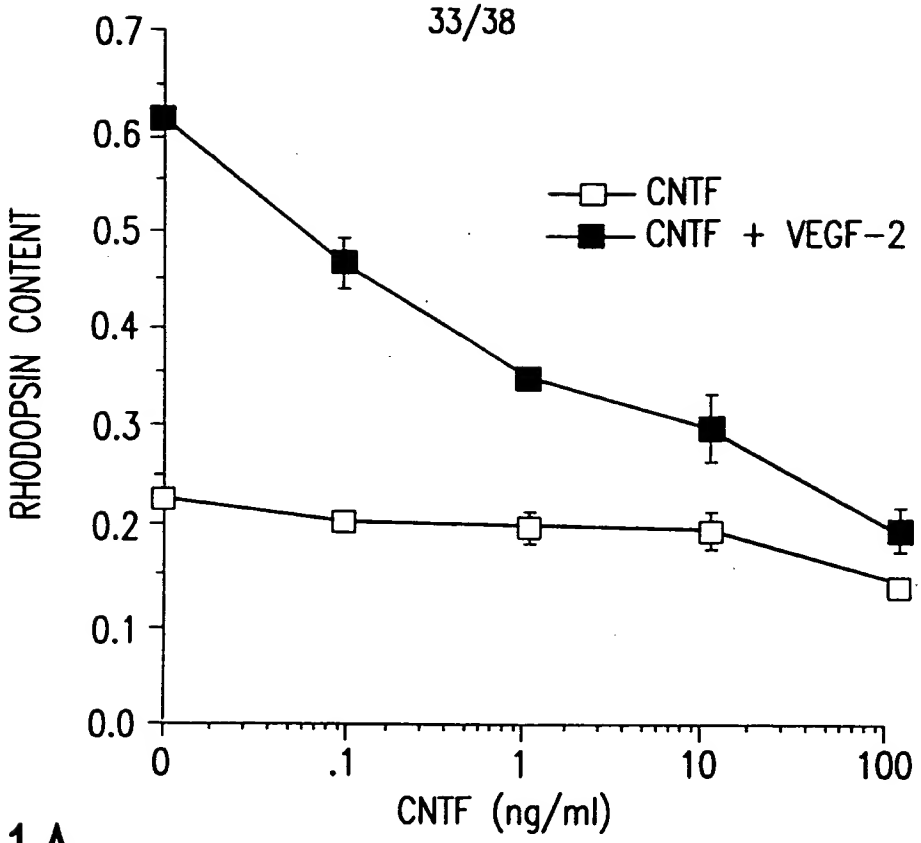

FIG.21A

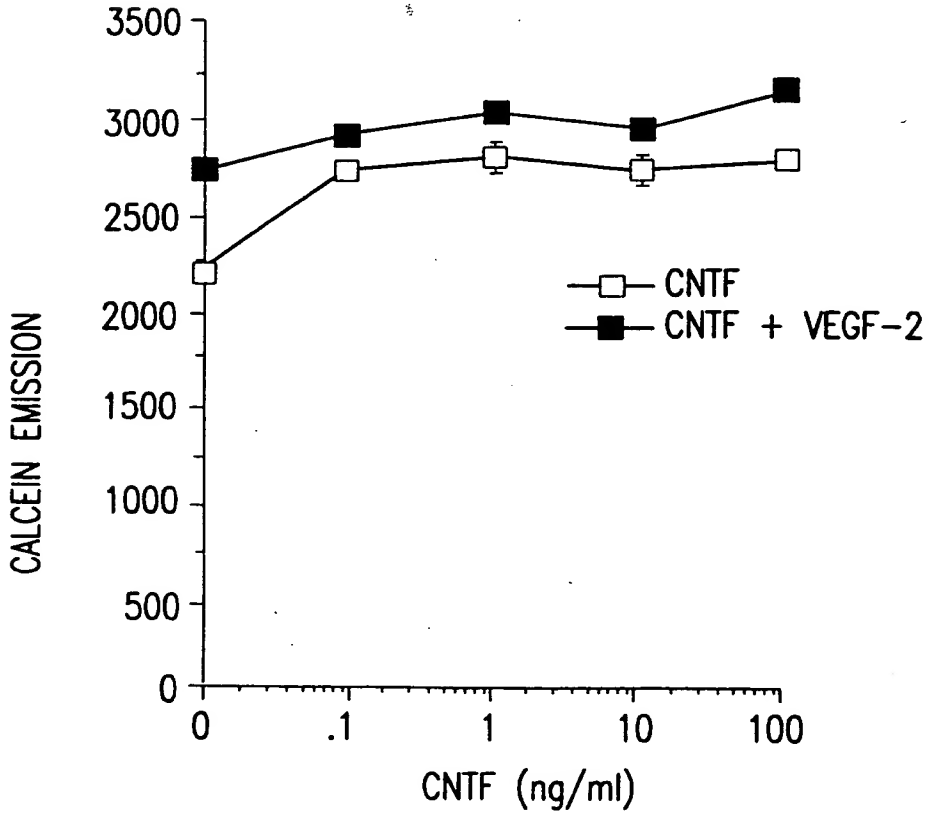

FIG.21B

OIPE JC
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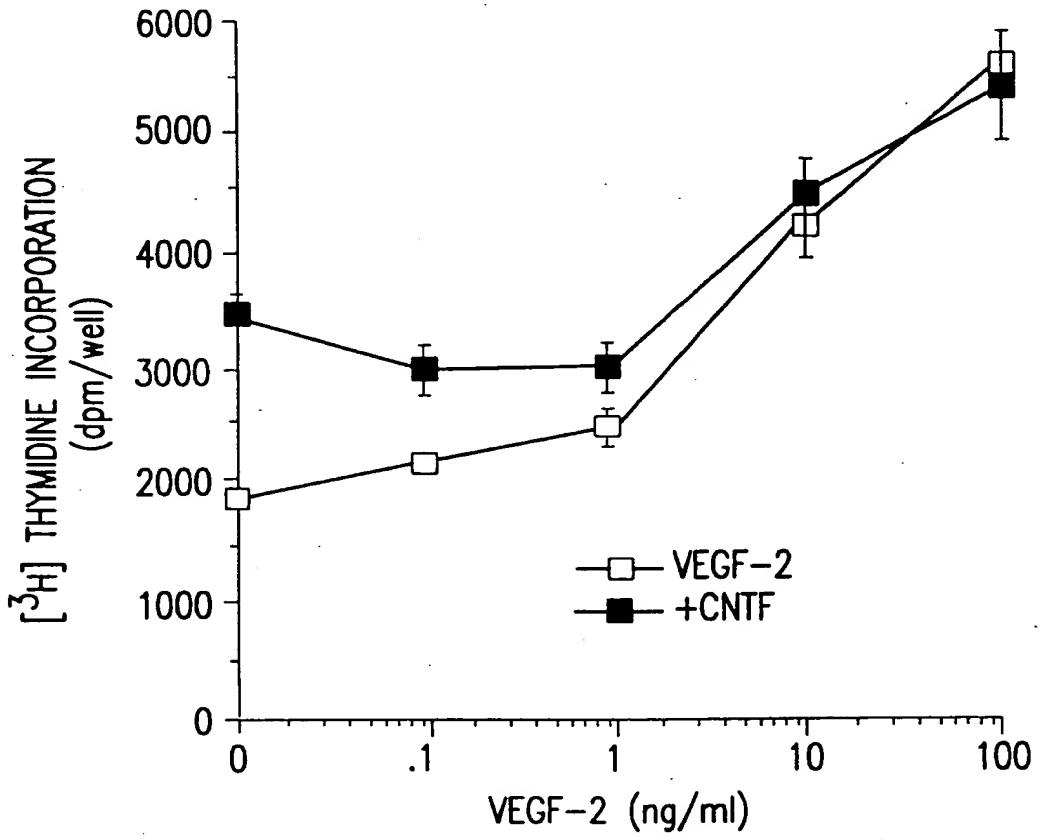

FIG.21C

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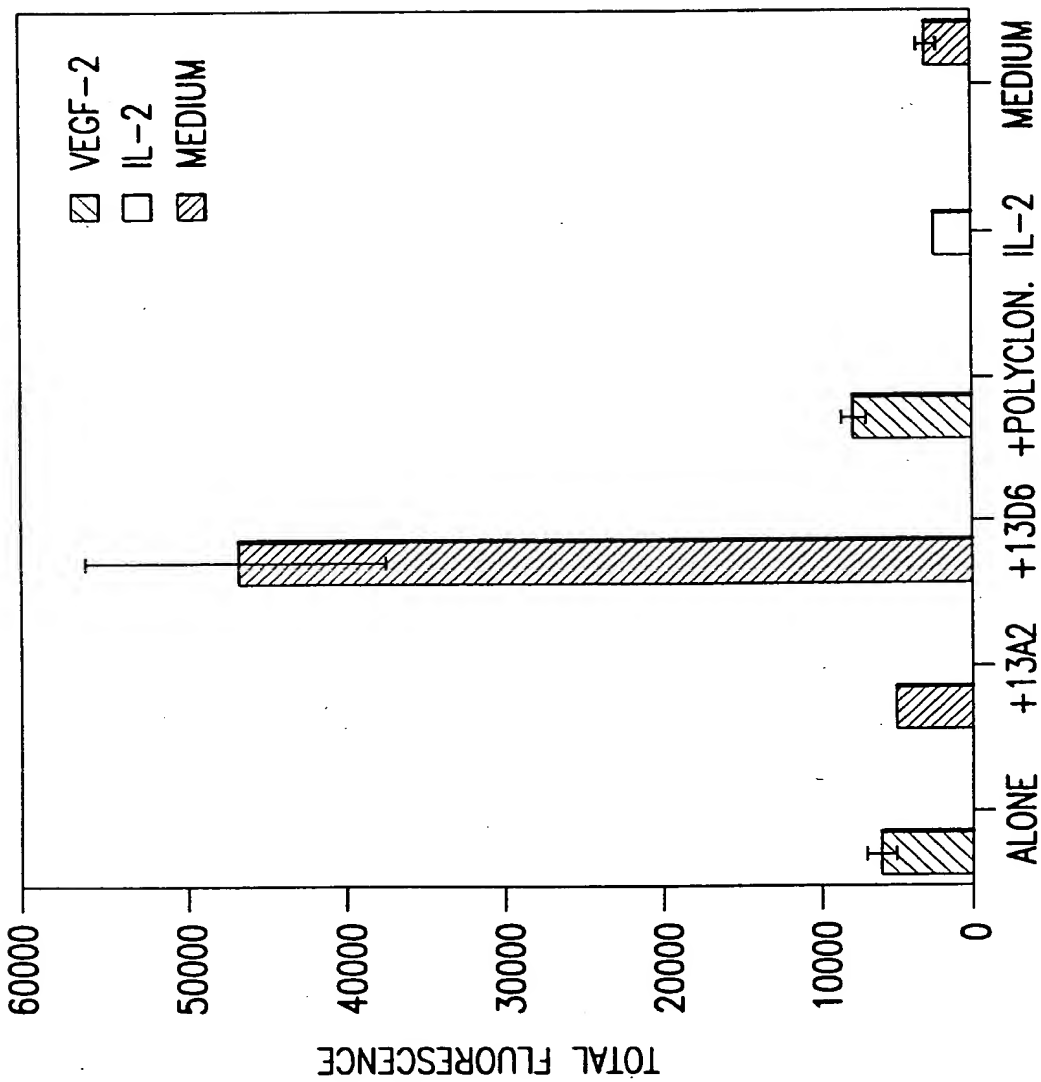

FIG.22

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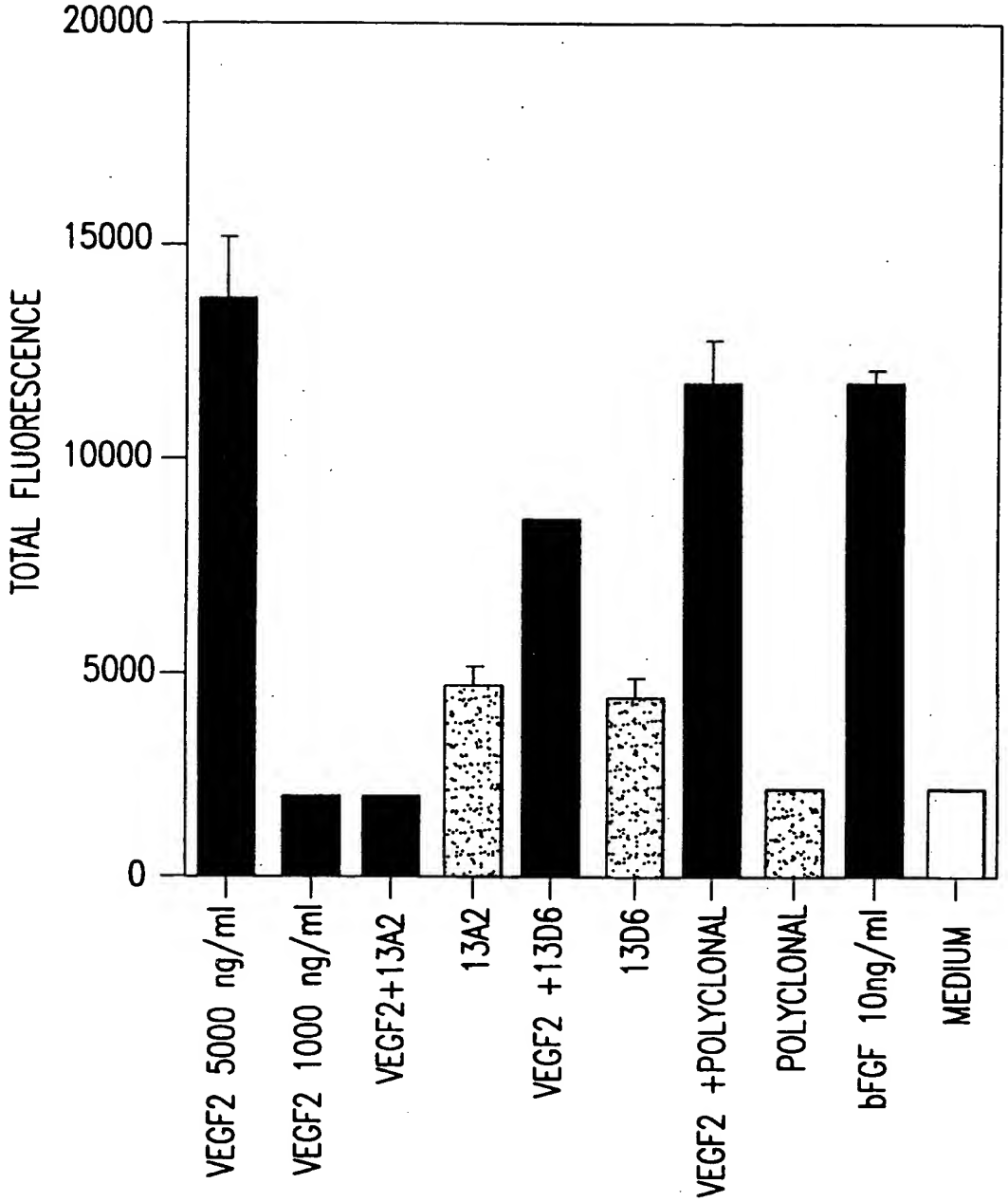

FIG.23

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EPITOPE MAP FOR MURINE ANTI VEGF-2 MAB

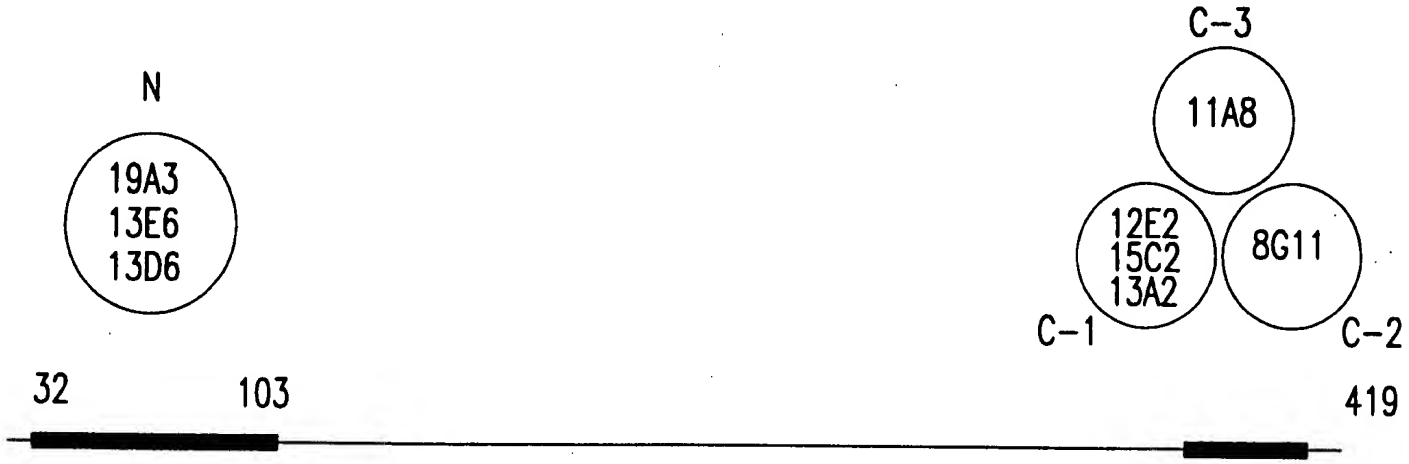

FIG.24

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MURINE VEGF-2 MAB STATUS

	ISOTYPE	REL. AFFINITY ng/ml	SPECIFICITY	REACTIVITY WESTERN	ELISA	PURIFIED mg
12E2	γ1	<1	C-1	+	+	27
13A2	γ1	<1	C-1	n.t	+	27
15C2	γ1	<1	C-1	n.t	+	10
13D6	γ1	<1	N	+	+	25
13E6	γ1	1	N	+	+	38
19A3	γ1	1	N	+	+	54
8G11	γ1	5	C-2	+	+	7
11A8	γ1	<1	C-3	+	+	9

FIG.25